

EXHIBIT "A"



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1: NP_620686. a disintegrin-like...[gi:21265058]

BLink, Domains, Links

LOCUS NP_620686 950 aa linear PRI 05-OCT-2003
 DEFINITION a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 15 preproprotein [Homo sapiens].
 ACCESSION NP_620686
 VERSION NP_620686.1 GI:21265058
 DBSOURCE REFSEQ: accession NM_139055.1
 KEYWORDS .
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (residues 1 to 950)
 AUTHORS Cal,S., Obaya,A.J., Llamazares,M., Garabaya,C., Quesada,V. and Lopez-Otin,C.
 TITLE Cloning, expression analysis, and structural characterization of seven novel human ADAMTSs, a family of metalloproteinases with disintegrin and thrombospondin-1 domains
 JOURNAL Gene 283 (1-2), 49-62 (2002)
 MEDLINE 21856482
 PUBMED 11867212
 COMMENT REVIEWED REFSEQ: This record has been curated by NCBI staff. The reference sequence was derived from AJ315733.1.

Summary: This gene encodes a member of the ADAMTS (a disintegrin and metalloproteinase with thrombospondin motifs) protein family. ADAMTS family members share several distinct protein modules, including a propeptide region, a metalloproteinase domain, a disintegrin-like domain, and a thrombospondin type 1 (TS) motif. Individual members of this family differ in the number of C-terminal TS motifs, and some have unique C-terminal domains. The protein encoded by this gene has a high sequence similarity to the proteins encoded by ADAMTS1 and ADAMTS8. The function of this protein has not been determined.

FEATURES Location/Qualifiers
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 /db_xref="taxon:9606"
 /chromosome="11"
 /map="11q25"
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 Region 67..180
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'cysteine switch' of the matrixins. This motif is found at the C terminus of the alignment but is not well aligned"
/note="Pep_M12B_propep"
/db_xref="CDD:pfam01562"
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206..950
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Region
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/note="Reprolysin"
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/note="ACR"
/db_xref="CDD:smart00608"
Region
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go_function: metalloendopeptidase activity [goid 0004222]
[evidence IEA];
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IEA];
go_process: integrin-mediated signaling pathway [goid
0007229] [evidence IEA];
go_process: proteolysis and peptidolysis [goid 0006508]
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181 npailraldp ykprragfge srssrrsgra krfvsipryv etlvvadesm vfkfhgadleh
241 ylltlataa rlyrhpsiln pinivvvkvl llrdrdsgpk vtgnaaltr nfcawqkkln
301 kvsdkhpeyw dtailftrqd lcgattcdtl gmadvgtmcd pkrscsvied dglpsaftta
361 helghvfnmp hdnvkvceev fgklranhmm sptliqidra npwsacsaaai itdfldsghg
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481 qtrhfpwadg tscgegkcl kgacverhn1 nkhrvdgswa kdpygpcsr tcgggvqlar
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601 vawvpkysgv sprdkcklic rangtgyfyv lapkvvdgtl cspdtsvcv qgkciagcd
661 gnlgskkrfd kcgvcggdnk sckvtglft kpmhgynfvv aipagassid irqrgykgli
721 gddnlylalkn sqgkyllngh fvvssaverdl vvkgsllyrs gtgtaveslq asrpileplt
781 vevlsvgkmt pprvrysfly pkepredkss hpkdprgpsv lhnsvlslsn qveqpddrpp
841 arwvagswgp csascgsglq kravdcrgsa gqrtvpacda ahrpvetqac gepcptwels
901 awspcskscg rgfqrrslkc vghggrllar dqcnlhkpkq eldfcvlrpc

//

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Nov 3 2003 07:26:36

FASTA searches a protein or DNA sequence data bank
version 3.3t05 March 30, 2000

Please cite:

W.R. Pearson & D.J. Lipman PNAS (1988) 85:2444-2448

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>Lex 241 SEQ ID NO:4  
vs /tmp/fastaNAAwSainL library  
searching /tmp/fastaNAAwSainL library
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950 residues in 1 sequences

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join: 39, opt: 27, gap-pen: -12/ -2, width: 16
Scan time: 0.017

The best scores are:
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Smith-Waterman score: 6692; 100.000% identity in 950 aa overlap (1-950:1-950)
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gi 212	MLLLGILTLAFA GRTAGGSEPEREV VVPIRLDPDINGR RYYWWRGPEDSGD QGLIFQITAF	10	20	30	40	50	60

	190	200	210	220	230	240
Lex	NPAILRALDPYKPRRAGFGE	RSRRSGRAKRFV	SIPRYVETLVVADE	SMVKFHGADLEH		

gi 212	NPAILRALDPYKPRRAGFGE	RSRRSGRAKRFV	SIPRYVETLVVADE	SMVKFHGADLEH		
	190	200	210	220	230	240

	250	260	270	280	290	300		
Lex	YLLTLLATAARLYRHPSILNPINIVVVKVLLLDRDSGPKVTGNAALT	RNFCAWQKKLN		
gi 212	YLLTLLATAARLYRHPSILNPINIVVVKVLLLDRDSGPKVTGNAALT	RNFCAWQKKLN	250	260	270	280	290	300

	310	320	330	340	350	360
Lex	KVSDKHPEYWDTAILFTRQDLCGATTCDTLGMADVGTMCDPKRSCSVIEDDGLPSAFTTA	⋮	⋮	⋮	⋮	⋮
gi 212	KVSDKHPEYWDTAILFTRQDLCGATTCDTLGMADVGTMCDPKRSCSVIEDDGLPSAFTTA	⋮	⋮	⋮	⋮	⋮

370 380 390 400 410 420
HEI CHYENMRPHDNVYKUCEEVECKL RANHMMSPRL TOLDRANPWSACSAALITDELDSCHG

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	gi 212	::: DCLLDQPSKPISLPEDLPGAS YTLSQQCELA FGVGSKPCPYM QYCTKLWCTG KAKGQMVC					
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Lex		490	500	510	520	530	540
	gi 212	::: QTRHFPWADGTSCGEGKLCLK GACVERHNLNKHRV DGSWAKWDPYGPCSRTCGGGVQLAR					
		490	500	510	520	530	540
Lex		550	560	570	580	590	600
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Lex		670	680	690	700	710	720
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Lex		730	740	750	760	770	780
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Lex		850	860	870	880	890	900
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	gi 212	::: AWSPCSKSCGRGFQRRSLKCVGHGGRL LARDQC NLH RKPQELDFC VLRPC					
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950 residues in 1 query sequences
950 residues in 1 library sequences
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Function used was FASTA